GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 31, 2005, 16:14:26 ; Search time 0.001 Seconds
(without alignments)
537.732 Million cell updates/sec

Title: us-10-063-553-47
Perfect score: 766
Sequence: 1 ggctcgagcgtttctgagcc.....agtagtttgaaaaaaaaaa 766

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 351 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : us-09-803-719-950:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	265.2	34.6	351	1	us-09-803-719-950	
c 2	21.6	2.8	351	1	us-09-803-719-950	

ALIGNMENTS

RESULT 1
us-09-803-719-950

Query Match 34.6%; Score 265.2; DB 1; Length 351;
Best Local Similarity 91.0%; Pred. No. 0;
Matches 303; Conservative 0; Mismatches 28; Indels 2; Gaps 2;

```
Qy          7 AGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGGA 66
              | || | ||| |||| | ||||||||||||||||  ||||||||||||||||    | |
Db         18 AACGCTCCTGTGCCATGCGTGACCATGACCTGCTGATAAGGATGGACATCCTGCCTAGTA 77

Qy         67 TTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCT-CTAATTGT 125
               ||| ||||||||  | ||||||||| ||||||| ||||||| ||||| |||| ||||||||
Db         78 CTCAACCTGCTGCCTTTACTGCTGGTAGGAGTCGTTCTCACTGCGACACCTGCTAATTGT 137

Qy        126 CAGCTTAGTT-GAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGT 184
              ||  ||| || |||||||||||||| |||||||| ||||||||||||||||||||||||
Db        138 CATATTATTTAGAGGAAGACCAATTGTCTCAAAAGCCCATCTCTTGCTTTGAGTGGTGGT 197

Qy        185 TCCCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAG 244
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TCCCACGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAG 257

Qy        245 CAAGAAAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTCAGTG 304
              ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        258 CAAGAAAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCACTTTTCAGTG 317
```

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Qy        305 TGATCACAGTCATTGGTGCTCTGTATTGCATGC 337
              |||||||||||||||||||||||||||||||||
Db        318 TGATCACAGTCATTGGTGCTCTGTATTGCATGC 350
```

RESULT 2
us-09-803-719-950/c

Query Match 2.8%; Score 21.6; DB 1; Length 351;
Best Local Similarity 51.0%; Pred. No. 0;
Matches 51; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

```
Qy        225 AACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTT 284
              | || ||||| |  |||   ||   ||||| |       | ||||    |  |    ||||
Db        337 AGCACCAATGACTGTGATCACACTGAAAAGTGATGAAAGAAACATTCCAGTTCTGTTGTT 278

Qy        285 TCTTTCATCATTTTTCAGTGTGATCACAGTCATTGGTGCT 324
               |      |  ||||   ||   |||  | |||||  || |
Db        277 GCAGCACGCTCTTTTTCTTGCTGTCAAGGACATTGTTGTT 238
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Search completed: January 31, 2005, 16:14:26
Job time : 0.001 secs

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 31, 2005, 16:18:13 ; Search time 0.001 Seconds
(without alignments)
438.152 Million cell updates/sec

Title: us-10-063-553-47
Perfect score: 766
Sequence: 1 ggctcgagcgtttctgagcc.....agtagtttgaaaaaaaaaaa 766

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 286 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : aaf98695.geneseqn2001bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	231.4	30.2	286	1	AAF98695	Human ovarian canc
c 2	16.6	2.2	286	1	AAF98695	Human ovarian canc

ALIGNMENTS

RESULT 1
AAF98695
ID AAF98695 standard; DNA; 286 BP.
XX
AC AAF98695;
XX
DT 02-JUL-2001 (first entry)
XX
DE Human ovarian cancer cell expressed sequence 10793.
XX
KW Human; ovarian cancer; identification; detection; characterisation;
KW tumour; kinase; marker; cytostatic; antisense gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200118542-A2.
XX
PD 15-MAR-2001.
XX
PF 01-SEP-2000; 2000WO-US024199.
XX
PR 03-SEP-1999; 99US-0152547P.
PR 16-MAR-2000; 2000US-0190347P.
PR 21-MAR-2000; 2000US-0191321P.
PR 31-MAY-2000; 2000US-0208382P.
PR 20-JUL-2000; 2000US-00220467.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lee J, Thompsho P, Lillie J;
XX
DR WPI; 2001-211428/21.
XX
PT Detection, assessment, prevention and therapy of ovarian cancer,
PT comprises detecting changes in the expression of a variety of markers.
XX
PS Claim 1; Page 998-999; 1198pp; English.
XX
CC The present invention describes a method for assessing whether a patient
CC is afflicted with ovarian cancer by comparing: (1) the expression of a
CC marker (I) (see AAF98594 to AAF98730), in a patient sample; and (2) the
CC normal level of expression of (I) in a control non-ovarian cancer sample,
CC where a significant difference between the level of expression in (a) and
CC (b) is an indication that the patient is afflicted with ovarian cancer.
CC (I) have cytostatic activities and can be used in antisense gene therapy.
CC The method, compositions and kits from the present invention can be used
CC for: (1) assessing and treating ovarian cancer; (2) making isolated
CC hybridoma, which produces an antibody useful for ovarian cancer
CC assessment; and (3) inhibiting ovarian cancer in a patient. AAF98573 to
CC AAF98593 represent human kinase marker primers and probes which are used
CC in the exemplification of the present invention
XX
SQ Sequence 286 BP; 65 A; 69 C; 76 G; 76 T; 0 U; 0 Other;

Query Match 30.2%; Score 231.4; DB 1; Length 286;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          7 AGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGGA 66
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         48 AACGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGGA 107

Qy         67 TTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        108 TTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTC 167

Qy        127 AGCTTAGTTGAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGTTC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 AGCTTAGTTGAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGTTC 227

Qy        187 CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTT 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTT 280
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RESULT 2
AAF98695/c
ID AAF98695 standard; DNA; 286 BP.
XX
AC AAF98695;
XX
DT 02-JUL-2001 (first entry)
XX
DE Human ovarian cancer cell expressed sequence 10793.
XX
KW Human; ovarian cancer; identification; detection; characterisation;
KW tumour; kinase; marker; cytostatic; antisense gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200118542-A2.
XX
PD 15-MAR-2001.
XX
PF 01-SEP-2000; 2000WO-US024199.
XX
PR 03-SEP-1999; 99US-0152547P.
PR 16-MAR-2000; 2000US-0190347P.
PR 21-MAR-2000; 2000US-0191321P.

PR 31-MAY-2000; 2000US-0208382P.
PR 20-JUL-2000; 2000US-00220467.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lee J, Thompsho P, Lillie J;
XX
DR WPI; 2001-211428/21.
XX
PT Detection, assessment, prevention and therapy of ovarian cancer,
PT comprises detecting changes in the expression of a variety of markers.
XX
PS Claim 1; Page 998-999; 1198pp; English.
XX
CC The present invention describes a method for assessing whether a patient
CC is afflicted with ovarian cancer by comparing: (1) the expression of a
CC marker (I) (see AAF98594 to AAF98730), in a patient sample; and (2) the
CC normal level of expression of (I) in a control non-ovarian cancer sample,
CC where a significant difference between the level of expression in (a) and
CC (b) is an indication that the patient is afflicted with ovarian cancer.
CC (I) have cytostatic activities and can be used in antisense gene therapy.
CC The method, compositions and kits from the present invention can be used
CC for: (1) assessing and treating ovarian cancer; (2) making isolated
CC hybridoma, which produces an antibody useful for ovarian cancer
CC assessment; and (3) inhibiting ovarian cancer in a patient. AAF98573 to
CC AAF98593 represent human kinase marker primers and probes which are used
CC in the exemplification of the present invention
XX
SQ Sequence 286 BP; 65 A; 69 C; 76 G; 76 T; 0 U; 0 Other;

Query Match 2.2%; Score 16.6; DB 1; Length 286;
Best Local Similarity 52.1%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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Qy        359 TAAAAGGTCCTCTCATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCAT 418
              | | ||||     || | | | |||| | || |||||   |||   |       | |||
Db        162 TTAGAGGTATCGCATTGAGAACTACTCCTAACAGCAGTAGAACCAGCAGGCTGAATCCAT 103

Qy        419 TGAAAAACATC 429
              || |  |  ||
Db        102 TGCAGGATGTC 92
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Search completed: January 31, 2005, 16:18:13
Job time : 0.001 secs

OM nucleic - nucleic search, using sw model

Run on: January 31, 2005, 16:16:07 ; Search time 0.001 Seconds
(without alignments)
1124.488 Million cell updates/sec

Title: us-10-063-553-47
Perfect score: 766
Sequence: 1 ggctcgagcgtttctgagcc.....agtagtttgaaaaaaaaaaa 766

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 734 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : aak88578.geneseqn2001as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	430.1	56.1	734	1	AAK88578	Human digestive sy
c	2	19	2.5	734	1	AAK88578	Human digestive sy

ALIGNMENTS

RESULT 1
AAK88578
ID AAK88578 standard; cDNA; 734 BP.
XX
AC AAK88578;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system antigen coding sequence SEQ ID NO: 894.
XX
KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW digestive system disorder; Meckel's diverticulum; ss.
XX
OS Homo sapiens.
XX
PN WO200155314-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001324.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-502630/55.
DR P-PSDB; AAM92805.
XX
PT Polynucleotides encoding digestive system antigens, useful for
PT diagnosing, treating, preventing and/or prognozing disorders of the
PT digestive system, particularly cancer and cancer metastases.
XX
PS Claim 1; SEQ ID NO 894; 986pp; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human digestive system antigens. These can be used in the
CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a cDNA encoding a digestive
CC system antigen of the invention
XX
SQ Sequence 734 BP; 214 A; 124 C; 155 G; 233 T; 0 U; 8 Other;

Query Match 56.1%; Score 430.1; DB 1; Length 734;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 440; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

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Qy        317 TTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTCATGT 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTCATGT 60

Qy        377 GTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACA 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACA 120

Qy        437 TTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG 180

Qy        497 GTTTCAATAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCC 556
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTTTCAATAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCC 240

Qy        557 ACTTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTTAGGTCTAT 616
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACTTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTTAGGTCTAT 300

Qy        617 TGCTTGTTGGAATTCTGGAGGTCCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTT- 675
              |||||||||||||||||||||||||||||||||||||||||||||||||||:||||:|
Db        301 TGCTTGTTGGAATTCTGGAGGTCCTGTTTGGGCTCAGTCAGATAGTCATCGGKTTCCYTG 360

Qy        676 GGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAA 735
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGCKGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAA 420

Qy        736 ATGTAAGTATCAGTAGTTTGAAAAAA 761
              |||||||||||||||||||||  ||
Db        421 ATGTAAGTATCAGTAGTTTGAATTAA 446
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RESULT 2
AAK88578/c
ID AAK88578 standard; cDNA; 734 BP.
XX
AC AAK88578;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system antigen coding sequence SEQ ID NO: 894.
XX
KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW digestive system disorder; Meckel's diverticulum; ss.
XX
OS Homo sapiens.
XX
PN WO200155314-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001324.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
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PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
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PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
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PR 02-OCT-2000; 2000US-0236802P.
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PR 20-OCT-2000; 2000US-0241785P.
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PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
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PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-502630/55.
DR P-PSDB; AAM92805.
XX
PT Polynucleotides encoding digestive system antigens, useful for
PT diagnosing, treating, preventing and/or prognozing disorders of the
PT digestive system, particularly cancer and cancer metastases.
XX
PS Claim 1; SEQ ID NO 894; 986pp; English.
XX

CC The present invention provides the protein and coding sequences of a
CC number of human digestive system antigens. These can be used in the
CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a cDNA encoding a digestive
CC system antigen of the invention
XX
SQ Sequence 734 BP; 214 A; 124 C; 155 G; 233 T; 0 U; 8 Other;

Query Match 2.5%; Score 19; DB 1; Length 734;
Best Local Similarity 51.8%; Pred. No. 0;
Matches 43; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

```
Qy        394 AGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTCATCCAGAATCCTTC 453
              | | ||  |||   ||| |||  |   ||    |    | | ||| || || | | ||
Db        489 AATCATCTCAAAGATGACTTTGAAAACAAGTGTACTTCTCAAATTAATTCAAACTACTGA 430

Qy        454 AACTTGCAGTGGTTTTTCAATGA 476
               |||| || |   ||  || | |
Db        429 TACTTACATTTTATTCCCATTAA 407
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Search completed: January 31, 2005, 16:16:08
Job time : 1 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 31, 2005, 16:17:18 ; Search time 0.001 Seconds
(without alignments)
537.732 Million cell updates/sec

Title: us-10-063-553-47
Perfect score: 766
Sequence: 1 ggctcgagcgtttctgagcc.....agtagtttgaaaaaaaaaa 766

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 351 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : aas37892.geneseqn2001as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	265.2	34.6	351	1	AAS37892	Novel human diagno
c 2	21.6	2.8	351	1	AAS37892	Novel human diagno

ALIGNMENTS

RESULT 1
AAS37892
ID AAS37892 standard; cDNA; 351 BP.
XX
AC AAS37892;
XX
DT 17-DEC-2001 (first entry)
XX
DE Novel human diagnostic and therapeutic gene #950.
XX
KW Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic; ss.
XX
OS Homo sapiens.
XX
PN WO200166753-A2.
XX
PD 13-SEP-2001.
XX
PF 09-MAR-2001; 2001WO-US007787.
XX
PR 09-MAR-2000; 2000US-0188609P.
XX
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
XX
PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Randazzo F, Kennedy GC, Pot D, Kassam A, Lamson G;
PI Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B;
XX
DR WPI; 2001-530177/58.
XX
PT New polynucleotides and polypeptides, useful for diagnosis and treatment
PT of breast, lung and colon cancer.
XX
PS Claim 1; Page 836; 1193pp; English.
XX
CC The invention relates to new polynucleotides and polypeptides, useful for
CC diagnosis and treatment of breast, lung and colon cancer. The sequences
CC can be used in detecting differentially expressed genes correlated with a
CC cancerous state of a mammalian cell, comprising detecting at least one
CC differentially expressed gene product in a test sample derived from a
CC cell suspected of being cancerous. They can also be used to inhibit
CC tumour growth by modulating expression of a gene product. AAS36943-
CC AAS39338 represent novel human diagnostic and therapeutic coding
CC sequences of the invention
XX
SQ Sequence 351 BP; 87 A; 86 C; 80 G; 97 T; 0 U; 1 Other;

Query Match 34.6%; Score 265.2; DB 1; Length 351;
Best Local Similarity 91.0%; Pred. No. 0;
Matches 303; Conservative 0; Mismatches 28; Indels 2; Gaps 2;

```
Qy          7 AGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGGA 66
              | || | ||| |||| | ||||||||||||||||||  ||||||||||||||||||   | |
Db         18 AACGCTCCTGTGCCATGCGTGACCATGACCTGCTGATAAGGATGGACATCCTGCCTAGTA 77

Qy         67 TTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCT-CTAATTGT 125
                ||| |||||||  | ||||||||  |||||||  |||||||  |||||  ||||  ||||||||
Db         78 CTCAACCTGCTGCCTTTACTGCTGGTAGGAGTCGTTCTCACTGCGACACCTGCTAATTGT 137

Qy        126 CAGCTTAGTT-GAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGT 184
              ||  ||| ||  |||||||||||||  ||||||||  |||||||||||||||||||||||||
Db        138 CATATTATTTAGAGGAAGACCAATTGTCTCAAAAGCCCATCTCTTGCTTTGAGTGGTGGT 197

Qy        185 TCCCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAG 244
              |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 TCCCACGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAG 257

Qy        245 CAAGAAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTCAGTG 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db        258 CAAGAAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCACTTTTCAGTG 317

Qy        305 TGATCACAGTCATTGGTGCTCTGTATTGCATGC 337
              |||||||||||||||||||||||||||||||||
Db        318 TGATCACAGTCATTGGTGCTCTGTATTGCATGC 350
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RESULT 2
AAS37892/c
ID AAS37892 standard; cDNA; 351 BP.
XX
AC AAS37892;
XX
DT 17-DEC-2001 (first entry)
XX
DE Novel human diagnostic and therapeutic gene #950.
XX
KW Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic; ss.
XX
OS Homo sapiens.
XX
PN WO200166753-A2.
XX
PD 13-SEP-2001.
XX
PF 09-MAR-2001; 2001WO-US007787.
XX
PR 09-MAR-2000; 2000US-0188609P.

XX
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
XX
PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Randazzo F, Kennedy GC, Pot D, Kassam A, Lamson G;
PI Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B;
XX
DR WPI; 2001-530177/58.
XX
PT New polynucleotides and polypeptides, useful for diagnosis and treatment
PT of breast, lung and colon cancer.
XX
PS Claim 1; Page 836; 1193pp; English.
XX
CC The invention relates to new polynucleotides and polypeptides, useful for
CC diagnosis and treatment of breast, lung and colon cancer. The sequences
CC can be used in detecting differentially expressed genes correlated with a
CC cancerous state of a mammalian cell, comprising detecting at least one
CC differentially expressed gene product in a test sample derived from a
CC cell suspected of being cancerous. They can also be used to inhibit
CC tumour growth by modulating expression of a gene product. AAS36943-
CC AAS39338 represent novel human diagnostic and therapeutic coding
CC sequences of the invention
XX
SQ Sequence 351 BP; 87 A; 86 C; 80 G; 97 T; 0 U; 1 Other;

Query Match 2.8%; Score 21.6; DB 1; Length 351;
Best Local Similarity 51.0%; Pred. No. 0;
Matches 51; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

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Qy        225 AACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTT 284
              | || ||||| |  |||   ||   ||||| |      | ||||    |  |    ||||
Db        337 AGCACCAATGACTGTGATCACACTGAAAAGTGATGAAAGAAACATTCCAGTTCTGTTGTT 278

Qy        285 TCTTTCATCATTTTTCAGTGTGATCACAGTCATTGGTGCT 324
               |      |  ||||   ||   |||  | ||||| || |
Db        277 GCAGCACGCTCTTTTTCTTGCTGTCAAGGACATTGTTGTT 238
```

Search completed: January 31, 2005, 16:17:18
Job time : 0.001 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 31, 2005, 16:19:09 ; Search time 0.001 Seconds
(without alignments)
579.096 Million cell updates/sec

Title: us-10-063-553-47
Perfect score: 766
Sequence: 1 ggctcgagcgtttctgagcc.....agtagtttgaaaaaaaaaa 766

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 378 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : aas38101.geneseqn2001as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		148.6	19.4	378	1	AAS38101	Novel human diagno
c 2		18	2.3	378	1	AAS38101	Novel human diagno

ALIGNMENTS

RESULT 1
AAS38101
ID AAS38101 standard; cDNA; 378 BP.
XX
AC AAS38101;
XX
DT 17-DEC-2001 (first entry)
XX
DE Novel human diagnostic and therapeutic gene #1159.
XX
KW Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic; ss.
XX
OS Homo sapiens.
XX
PN WO200166753-A2.
XX
PD 13-SEP-2001.
XX
PF 09-MAR-2001; 2001WO-US007787.
XX
PR 09-MAR-2000; 2000US-0188609P.
XX
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
XX
PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Randazzo F, Kennedy GC, Pot D, Kassam A, Lamson G;
PI Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B;
XX
DR WPI; 2001-530177/58.
XX
PT New polynucleotides and polypeptides, useful for diagnosis and treatment
PT of breast, lung and colon cancer.
XX
PS Claim 1; Page 887; 1193pp; English.
XX
CC The invention relates to new polynucleotides and polypeptides, useful for
CC diagnosis and treatment of breast, lung and colon cancer. The sequences
CC can be used in detecting differentially expressed genes correlated with a
CC cancerous state of a mammalian cell, comprising detecting at least one
CC differentially expressed gene product in a test sample derived from a
CC cell suspected of being cancerous. They can also be used to inhibit
CC tumour growth by modulating expression of a gene product. AAS36943-
CC AAS39338 represent novel human diagnostic and therapeutic coding
CC sequences of the invention
XX
SQ Sequence 378 BP; 112 A; 75 C; 73 G; 118 T; 0 U; 0 Other;

Query Match 19.4%; Score 148.6; DB 1; Length 378;
Best Local Similarity 89.4%; Pred. No. 0;
Matches 160; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy      158 ACCCCATCTCTTGCTTTGAGTGGTGGTTCCCAGGAATTATAGGAGCAGGTCTGATGGCCA 217
            |||||||||||||||||||||||| |  ||||| |||||||||||| |||| ||||||| ||
Db      199 ACCCCATCTCTTGCTTTGAGTGGGGCGTCCCAAGAATTATAGGAACAGGGCTGATGGGCA 258

Qy      218 TTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTGCTGCAACAACAGAACTG 277
            || |||| |||||||||||||||||| ||| ||||||| |||||| |||||||||||| ||
Db      259 TTTCAGCCACAACAATGTCCTTGACAACAAAAAAAAGATCGTGCTTCAACAACAGAAATG 318

Qy      278 GAATGTTTCTTTCATCATTTTTCAGTGTGATCACAGTCATTGGTGCTCTGTATTGCATG 336
            |||||||||||| |||| |||||||||||||||||||||||||| |||||| |||||||||
Db      319 CAATGTTTCTTTTATCACTTTTCAGTGTGATCACAGTCATTGGCGCTCTGGATTGCATG 377
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RESULT 2
AAS38101/c
ID AAS38101 standard; cDNA; 378 BP.
XX
AC AAS38101;
XX
DT 17-DEC-2001 (first entry)
XX
DE Novel human diagnostic and therapeutic gene #1159.
XX
KW Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic; ss.
XX
OS Homo sapiens.
XX
PN WO200166753-A2.
XX
PD 13-SEP-2001.
XX
PF 09-MAR-2001; 2001WO-US007787.
XX
PR 09-MAR-2000; 2000US-0188609P.
XX
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
XX
PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Randazzo F, Kennedy GC, Pot D, Kassam A, Lamson G;
PI Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B;
XX
DR WPI; 2001-530177/58.
XX
PT New polynucleotides and polypeptides, useful for diagnosis and treatment

PT of breast, lung and colon cancer.
XX
PS Claim 1; Page 887; 1193pp; English.
XX
CC The invention relates to new polynucleotides and polypeptides, useful for
CC diagnosis and treatment of breast, lung and colon cancer. The sequences
CC can be used in detecting differentially expressed genes correlated with a
CC cancerous state of a mammalian cell, comprising detecting at least one
CC differentially expressed gene product in a test sample derived from a
CC cell suspected of being cancerous. They can also be used to inhibit
CC tumour growth by modulating expression of a gene product. AAS36943-
CC AAS39338 represent novel human diagnostic and therapeutic coding
CC sequences of the invention
XX
SQ Sequence 378 BP; 112 A; 75 C; 73 G; 118 T; 0 U; 0 Other;

Query Match 2.3%; Score 18; DB 1; Length 378;
Best Local Similarity 49.0%; Pred. No. 0;
Matches 48; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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Qy        225 AACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTT 284
              | |  ||||| |  |||   ||   ||||| |      | ||||    |  |    ||||
Db        365 AGCGCCAATGACTGTGATCACACTGAAAAGTGATAAAAGAAACATTGCATTTCTGTTGTT 306

Qy        285 TCTTTCATCATTTTTCAGTGTGATCACAGTCATTGGTG 322
                      ||||   |||  |||  | ||||| ||
Db        305 GAAGCACGATCTTTTTTTTGTTGTCAAGGACATTGTTG 268
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Search completed: January 31, 2005, 16:19:09
Job time : 0.001 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 31, 2005, 16:21:35 ; Search time 0.001 Seconds
(without alignments)
91.920 Million cell updates/sec

Title: us-10-063-553-47
Perfect score: 766
Sequence: 1 ggctcgagcgtttctgagcc.....agtagtttgaaaaaaaaaaa 766

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 60 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : abn47584.geneseqn2002as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		60	7.8	60	1	ABN47584	Human spliced tran
c	2	9.8	1.3	60	1	ABN47584	Human spliced tran

ALIGNMENTS

RESULT 1
ABN47584
ID ABN47584 standard; DNA; 60 BP.
XX
AC ABN47584;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:20332.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
PS Example 1; SEQ ID NO 20332; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridising selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 60 BP; 16 A; 14 C; 16 G; 14 T; 0 U; 0 Other;

Query Match 7.8%; Score 60; DB 1; Length 60;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      513 CAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGA 572
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 CAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGA 60
```

RESULT 2
ABN47584/c
ID ABN47584 standard; DNA; 60 BP.
XX
AC ABN47584;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:20332.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
PS Example 1; SEQ ID NO 20332; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridising selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 60 BP; 16 A; 14 C; 16 G; 14 T; 0 U; 0 Other;

Query Match 1.3%; Score 9.8; DB 1; Length 60;
Best Local Similarity 58.6%; Pred. No. 0;
Matches 17; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```
Qy        477 CTCTTGTGCACCTCCTACTGGTTTCAATA 505
              ||||   ||  |||    |||| ||  ||
Db         32 CTCTCCAGCCACTCGCCATGGTGTCGTTA 4
```

Search completed: January 31, 2005, 16:21:35
Job time : 0.001 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 31, 2005, 16:20:13 ; Search time 0.001 Seconds
(without alignments)
162.392 Million cell updates/sec

Title: us-10-063-553-47
Perfect score: 766
Sequence: 1 ggctcgagcgtttctgagcc.....agtagtttgaaaaaaaaaaa 766

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 106 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : abs72969.geneseqn2002as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	70	9.1	106	1	ABS72969	Human gene trapped
c 2	15.8	2.1	106	1	ABS72969	Human gene trapped

ALIGNMENTS

RESULT 1
ABS72969
ID ABS72969 standard; cDNA; 106 BP.
XX
AC ABS72969;
XX
DT 03-DEC-2002 (first entry)
XX
DE Human gene trapped sequence (GTS) #929.
XX
KW Human; gene trapped sequence; GTS; gene; ss; cancer; autoimmune disease;
KW lupus; scleroderma; Crohn's disease; multiple sclerosis; immune disorder;
KW inflammatory bowel disease; schizophrenia; psychosis; osteoarthritis;
KW inflammatory disorder; diabetes; skin disorder; acne; eczema; asthma;
KW rheumatoid arthritis; hypertension; atherosclerosis; Alzheimer's disease;
KW cardiovascular disease; Parkinson's disease; osteoporosis; infertility;
KW viral infection; parasitic infection; fungal infection;
KW bacterial infection; forensic analysis; cellular differentiation.
XX
OS Homo sapiens.
XX
PN US2002095031-A1.
XX
PD 18-JUL-2002.
XX
PF 03-MAY-2000; 2000US-00563817.
XX
PR 04-MAY-1999; 99US-0132343P.
XX
PA (NEHL/) NEHLS M C.
PA (ZAMB/) ZAMBROWICZ B.
PA (SAND/) SANDS A T.
XX
PI Nehls MC, Zambrowicz B, Sands AT;
XX
DR WPI; 2002-656030/70.
XX
PT New isolated or purified human gene trapped sequences, useful for gene
PT discovery, as markers for gene expression analysis, identifying and
PT mapping the coding regions of human genome, or determining the genetic
PT basis of human disease.
XX
PS Claim 1; SEQ ID NO 937; 36pp; English.
XX
CC The invention relates to isolated or purified polynucleotides that
CC correspond to human gene trapped sequences (GTSs). The human GTSs are
CC useful for gene discovery and as markers for gene expression analysis,
CC for identifying and mapping the coding regions of the mammalian,
CC particularly human, genome, for forensic analysis, and for determining
CC the genetic basis of human disease. The peptides and proteins encoded by
CC the polynucleotides are useful for generating antibodies, as reagents in
CC diagnostic assays and in identifying other cellular gene products
CC involved in the regulation of development and cellular differentiation of
CC various cell types. The peptides are also useful as reagents in assays
CC for screening of compounds used in treating disorders affecting
CC development and cell differentiation. The GTSs are also useful in
CC treating or ameliorating diseases associated with the expression of
CC mutant or normal variants of the GTSs, e.g. cancer, autoimmune diseases,
CC lupus, scleroderma, Crohn's disease, multiple sclerosis, inflammatory
CC bowel disease, immune disorders, schizophrenia, psychosis, inflammatory
CC disorders, diabetes, skin disorders such as acne or eczema,
CC osteoarthritis, rheumatoid arthritis, hypertension, atherosclerosis,
CC cardiovascular diseases, Alzheimer's disease, Parkinson's disease,
CC osteoporosis, asthma, infertility, and viral, parasitic, fungal or
CC bacterial infections. This sequence represents a human GTS of the
CC invention
XX
SQ Sequence 106 BP; 26 A; 21 C; 28 G; 26 T; 0 U; 5 Other;

Query Match 9.1%; Score 70; DB 1; Length 106;
Best Local Similarity 88.7%; Pred. No. 0;
Matches 94; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

```
Qy        236 CCTTGACAGCAAGAAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCAT-CA 294
              |||||||||| |||||||||| ||||| ||| |||||||||||| || |||||| ||
Db          1 CCTTGACAGCAGGAAAAAGAGCGGGCTGCNACANCAGAACTGGAATGGTTNTTTCATGCA 60

Qy        295 TTTTTCAGTGTGA-TCACAGTCATTGGTGCTCTGTATTGCATGCTG 339
              ||||||||| ||  |||||||||||| ||||||||||||||||||
Db         61 CTTTTCAGTGNGAGACACAGTCATTGGNGCTCTGTATTGCATGCTG 106
```

RESULT 2
ABS72969/c
ID ABS72969 standard; cDNA; 106 BP.
XX
AC ABS72969;
XX
DT 03-DEC-2002 (first entry)
XX
DE Human gene trapped sequence (GTS) #929.
XX
KW Human; gene trapped sequence; GTS; gene; ss; cancer; autoimmune disease;
KW lupus; scleroderma; Crohn's disease; multiple sclerosis; immune disorder;
KW inflammatory bowel disease; schizophrenia; psychosis; osteoarthritis;
KW inflammatory disorder; diabetes; skin disorder; acne; eczema; asthma;
KW rheumatoid arthritis; hypertension; atherosclerosis; Alzheimer's disease;
KW cardiovascular disease; Parkinson's disease; osteoporosis; infertility;
KW viral infection; parasitic infection; fungal infection;

KW bacterial infection; forensic analysis; cellular differentiation.
XX
OS Homo sapiens.
XX
PN US2002095031-A1.
XX
PD 18-JUL-2002.
XX
PF 03-MAY-2000; 2000US-00563817.
XX
PR 04-MAY-1999; 99US-0132343P.
XX
PA (NEHL/) NEHLS M C.
PA (ZAMB/) ZAMBROWICZ B.
PA (SAND/) SANDS A T.
XX
PI Nehls MC, Zambrowicz B, Sands AT;
XX
DR WPI; 2002-656030/70.
XX
PT New isolated or purified human gene trapped sequences, useful for gene
PT discovery, as markers for gene expression analysis, identifying and
PT mapping the coding regions of human genome, or determining the genetic
PT basis of human disease.
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PS Claim 1; SEQ ID NO 937; 36pp; English.
XX
CC The invention relates to isolated or purified polynucleotides that
CC correspond to human gene trapped sequences (GTSs). The human GTSs are
CC useful for gene discovery and as markers for gene expression analysis,
CC for identifying and mapping the coding regions of the mammalian,
CC particularly human, genome, for forensic analysis, and for determining
CC the genetic basis of human disease. The peptides and proteins encoded by
CC the polynucleotides are useful for generating antibodies, as reagents in
CC diagnostic assays and in identifying other cellular gene products
CC involved in the regulation of development and cellular differentiation of
CC various cell types. The peptides are also useful as reagents in assays
CC for screening of compounds used in treating disorders affecting
CC development and cell differentiation. The GTSs are also useful in
CC treating or ameliorating diseases associated with the expression of
CC mutant or normal variants of the GTSs, e.g. cancer, autoimmune diseases,
CC lupus, scleroderma, Crohn's disease, multiple sclerosis, inflammatory
CC bowel disease, immune disorders, schizophrenia, psychosis, inflammatory
CC disorders, diabetes, skin disorders such as acne or eczema,
CC osteoarthritis, rheumatoid arthritis, hypertension, atherosclerosis,
CC cardiovascular diseases, Alzheimer's disease, Parkinson's disease,
CC osteoporosis, asthma, infertility, and viral, parasitic, fungal or
CC bacterial infections. This sequence represents a human GTS of the
CC invention
XX
SQ Sequence 106 BP; 26 A; 21 C; 28 G; 26 T; 0 U; 5 Other;

Query Match 2.1%; Score 15.8; DB 1; Length 106;
Best Local Similarity 74.1%; Pred. No. 0;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy         69 CAGCCTGCTGGTTCTACTGCTGTTAGG 95
              ||||| |||  || | ||||||| | |
Db         28 CAGCCCGCTCTTTTTCCTGCTGTCAAG 2
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Search completed: January 31, 2005, 16:20:13
Job time : 0.001 secs